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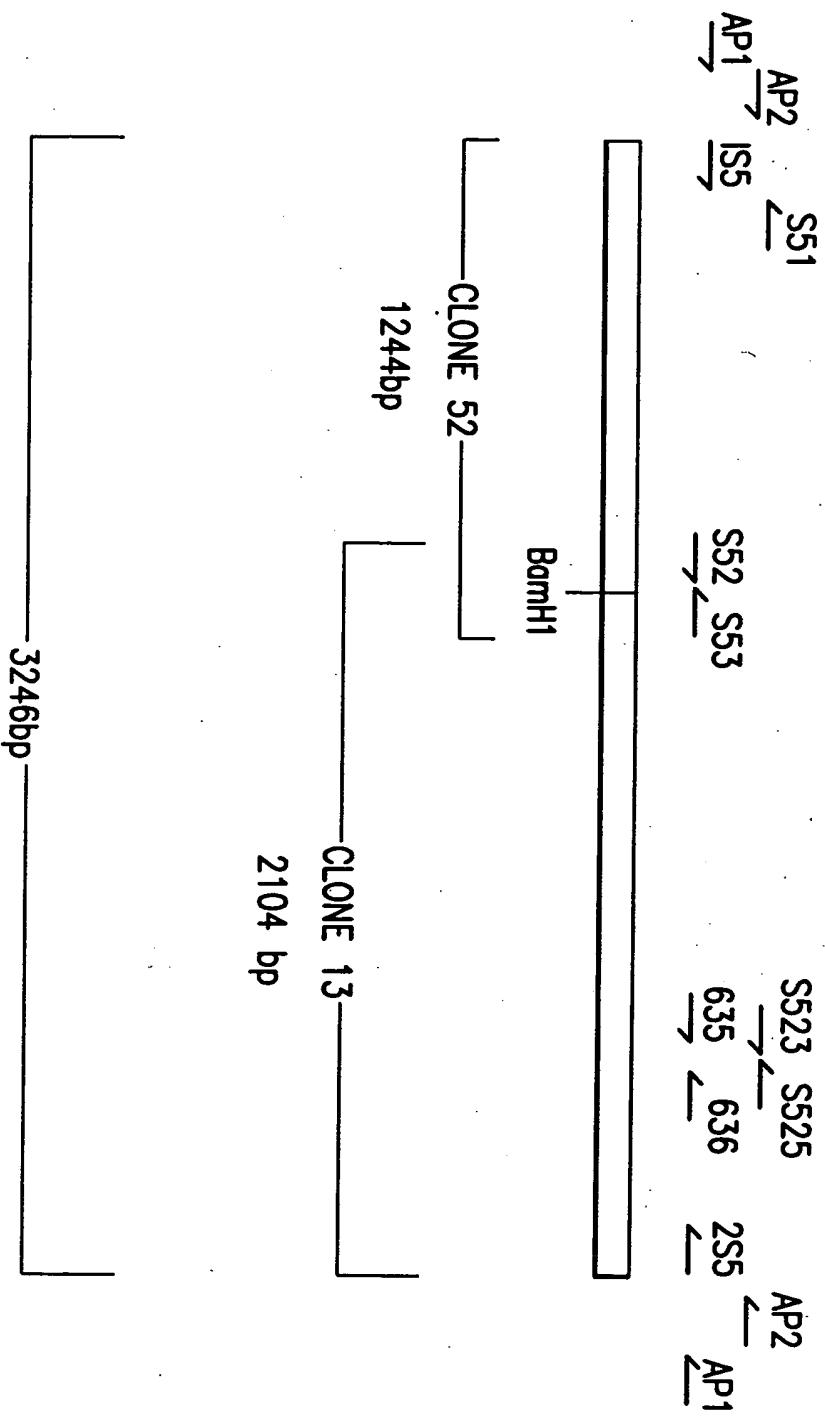
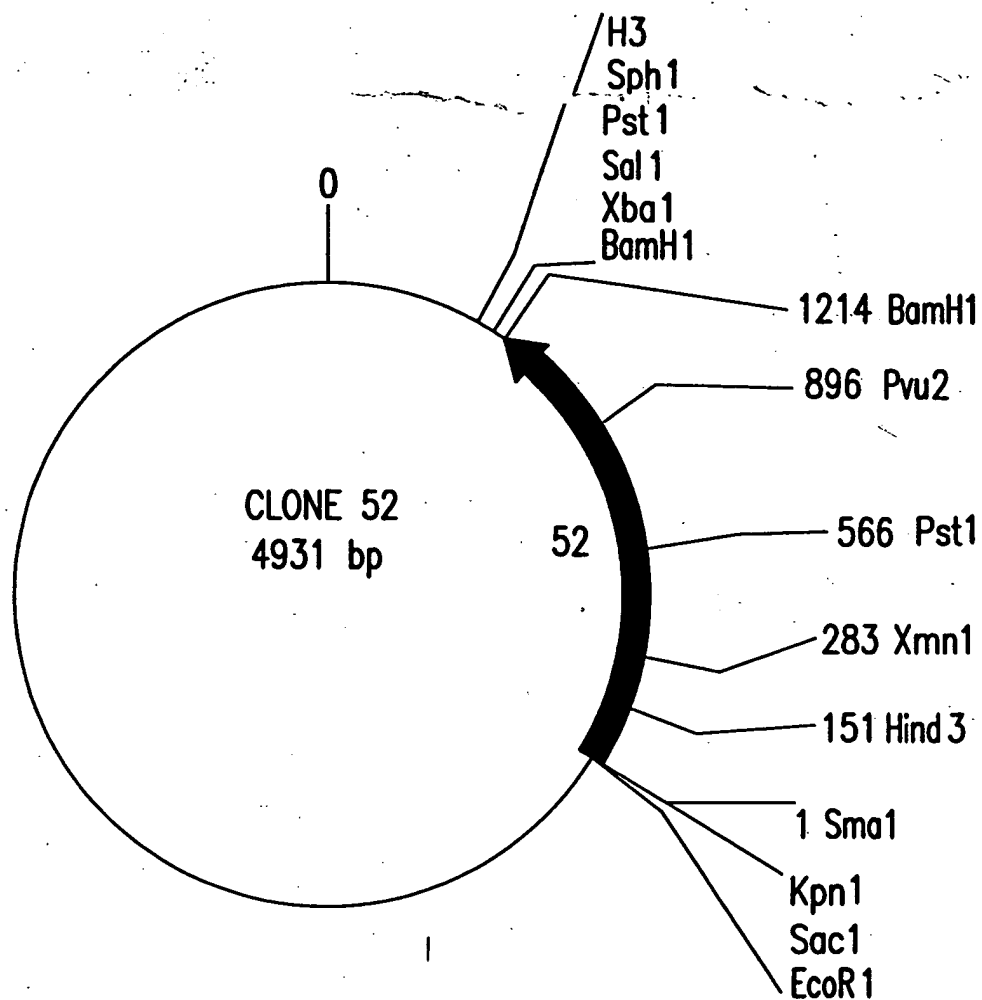
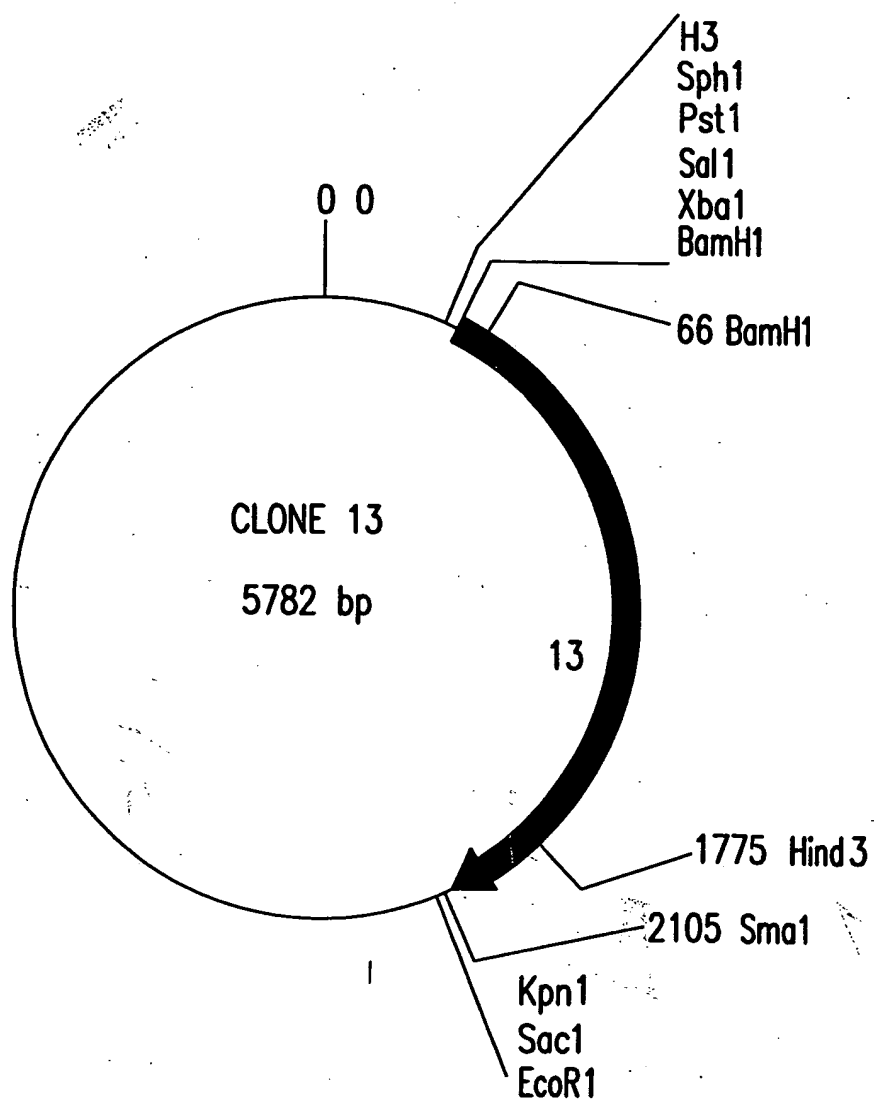


FIG.1



COMMENTS/REFERENCES: 52=3' SIDE OF S5 (AtMSH3) 1244bp IN pUC18/Sma1

FIG.2



COMMENTS/REFERENCES: 13=3' SIDE OF S5 (AtMSH3) 2104bp IN pUC18/Sma1

FIG.3

1	CCTAAGAAAGCGCGGAAAAATTGGCAACCCCAAGTTCGCCATAGCCACGACCACGACCCTTCCAATTTCTCTTAACGGAGGA	80
81	GATTACGAATAAGCAATT ATG GGC AAG CAA AAG CAG CAG ACG ATT TCT CGT TTC GCT CCC	144
1	M G K Q K Q Q T I S R F F A P	15
145	AAA CCC AAA TCC CCG ACT CAC GAA CCG AAT CCG GTA GCC GAA TCA TCA ACA CCG CCA CCG	204
16	K P K S P T H E P N P V A E S S T P P P	35
205	AAG ATA TCC GCC ACT GTA TCC TTC TCT CCT TCC AAG CGT AAG CTT CTC TCC GAC CAC CTC	264
36	K I S A T V S F S P S K R K L L S D H L	55
265	GCC GCC GCG TCA CCC AAA AAG CCT AAA CTT TCT CCT CAC ACT CAA AAC CCA GTA CCC GAT	324
56	A A A S P K K P K L S P H T Q N P V P D	75
325	CCC AAT TTA CAC CAA AGA TTT CTC CAG AGA TTT CTG GAA CCC TCG CCG GAG GAA TAT GTT	384
76	P N L H Q R F L Q R F L E P S P E E Y V	95
385	CCC GAA ACG TCA TCA TCG AGG AAA TAC ACA CCA TTG GAA CAG CAA GTG GTG GAG CTA AAG	444
96	P E T S S S R K Y T P L E Q Q V V E L K	115
445	AGC AAG TAC CCA GAT GTG GTT TTG ATG GTG GAA GTT GGT TAC AGG TAC AGA TTC TTC GGA	504
116	S K Y P D V V L M V E V G Y R Y R F F G	135
505	GAA GAC GCG GAG ATC GCA GCA CGC GTG TTG GGT ATT TAC GCT CAT ATG GAT CAC AAT TTC	564
136	E D A E I A A R V L G I Y A H M D H N F	155
565	ATG ACG GCG AGT GTG CCA ACA TTT CGA TTG AAT TTC CAT GTG AGA AGA CTG GTG AAT GCA	624
156	M T A S V P T F R L N F H V R R L V N A	175

FIG.4A

625	GGA TAC AAG ATT GGT GTA GTG AAG CAG ACT GAA ACT GCA GCC ATT AAG TCC CAT GGT GCA	684
176	G Y K I G V V K Q T E T A A I K S H G A	195
665	AAC CGG ACC GGC CCT TTT TTC CGG GGA CTG TCG GCG TTG TAT ACC AAA GCC ACG CTT GAA	744
196	N R T G P F F R G L S A L Y T K A T L E	215
745	GCG GCT GAG GAT ATA AGT GGT GGT TGT GGT GGT GAA GAA GGT TTT GGT TCA CAG AGT AAT	804
216	A A E D I S G G C G G E E G F G S Q S N	235
805	TTC TTG GTT TGT GTT GTT GTG GAT GAG AGA GTT AAG TCG GAG ACA TTA GGC TGT GGT ATT GAA	864
236	F L V C V V D E R V K S E T L G C G I E	255
865	ATG AGT TTT GAT GTT AGA GTC GGT GTT GTT GGC GTT GAA ATT TCG ACA GGT GAA GTT GTT	924
256	M S F D V R V G V V G V E I S T G E V V	275
925	TAT GAA GAG TTC AAT GAT AAT AAT TTC ATG AGA AGT GGA TTA GAG GCT GTG ATT TTG AGC TTG	9884
276	Y E E F N D N F M R S G L E A V I L S L	295
985	TCA CCA GCT GAG CTG TTG CTT GGC CAG CCT CTT TCA CAA CAA ACT GAG AAG TTT TTG GTG	1044
296	S P A E L L L G Q P L S Q Q T E K F L V	315
1045	GCA CAT GCT GGA CCT ACC TCA AAC GTT CGA GTG GAA CGT GCC TCA CTG GAT TGT TTC AGC	1104
316	A H A G P T S N V R V E R A S L D C F S	335
1105	AAT GGT AAT GCA GTA GAT GAG GTT ATT TCA TTA TGT GAA AAA ATC AGC GCA GGT AAC TTA	1164
336	N G N A V D E V I S L C E K I S A G N L	355
1165	GAA GAT GAT AAA GAA ATG AAG CTG GAG GCT GCT GAA AAA GGA ATG TCT TGC TTG ACA GTT	1224
356	E D D K E M K L E A A E K G M S C L T V	375

FIG.4B

1225	CAT ACA ATT ATG AAC ATG CCA CAT CTG ACT GTT CAA GCC CTC GCC CTA ACG TTT TGC CAT	1284
376	H T I M N M P H L T V Q A L A L T F C H	395
1285	CTC AAA CAG TTT GGA TTT GAA AGG ATC CTT TAC CAA GGG GCC TCA TTT CGC TCT TTG TCA	1344
396	L K Q F G F E R I L Y Q G A S F R S L S	415
1245	AGT AAC ACA GAG ATG ACT CTC TCA GCC AAT ACT CTG CAA CAG TTG GAG GTT GTG AAA AAT	1404
416	S N T E M T L S A N T L Q Q L E V V K N	435
1405	AAT TCA GAT GGA TCG GAA TCT GGC TCC TTA TTC CAT AAT ATG AAT CAC ACA CTT ACA GTA	1464
436	N S D G S E S G S L F H N M N H T L T V	455
1465	TAT GCT TCC AGG CTT CTT AGA CAC TGG GTG ACT CAT CCT CTA TGC GAT AGA AAT TTG ATA	1524
456	Y A S R L L R H W V T H P L C D R N L I	475
1525	TCT GCT CGG CTT GAT GCT GTT TCT GAG ATT TCT GCT TGC ATG GGA TCT CAT AGT TCT TCC	1584
476	S A R L D A V S E I S A C M G S H S S S	495
1585	CAG CTC AGC AGT GAG TTG GTT GAA GAA GGT TCT GAG AGA GCA ATT GTA TCA CCT GAG TTT	1644
496	Q L S S E L V E E G S E R A I V S P E F	515
1645	TAT CTC GTG CTC TCC TCA GTC TTG ACA GCT ATG TCT AGA TCA TCT GAT ATT CAA CGT GGA	1704
516	Y L V L L S S V L T A M S R S S D I Q R G	535
1705	ATA ACA AGA ATC TTT CAT CGG ACT GCT AAA GCC ACA GAG TTC ATT GCA GTT ATG GAA GCT	1764
536	I T R I F H R T A K A T E F I A V M E A	555
1765	ATT TTA CTT GCG GGG AAG CAA ATT CAG CGG CTT GGC ATA AAG CAA GAC TCT GAA ATG AGG	1824
556	I L L A G K Q I Q R L G I K Q D S E M R	575

FIG.4C

1825	AGT ATG CAA TGT GCA ACT GTG CGA TCT ACT CTT TTG AGA AAA TTG ATT TCT GTT ATT TCA	1884
576	S M Q S A T V R S T L L R K L I S V I S	595
1885	TCC CCT GTT GTG GTT GAC AAT GCC GGA AAA CTT CTC TCT GCC CTA AAT AAG GAA GCG GCT	1944
596	S P V V V D N A G K L L S A L N K E A A	615
1945	GTT CGA GGT GAC TTG CTC GAC ATA CTA ATC ACT TCC AGC GAC CAA TTT CCT GAG CTT GCT	2004
616	V R G D L L D I L I T S S D Q F P E L A	635
2005	GAA GCT CGC CAA GCA GTT TTA GTC ATC AGG GAA AAG CTG GAT TCC TCG ATA GCT TCA TTT	2064
636	E A R Q A V L V I R E K L D S S I A S F	655
2065	CGC AAG AAG CTC GCT ATT CGA AAT TTG GAA TTT CTT CAA GTG TCG GGG ATC ACA CAT TTG	2124
656	R K K L A I R N L E F L Q V S G I T H L	675
2125	ATA GAG CTG CCC GTT GAT TCC AAG GTC CCT ATG AAT TGG GTG AAA GTA AAT AGC ACC AAG	2184
676	I E L P V D S K V P M N W V K V N S T K	695
2185	AAG ACT ATT CGA TAT CAT CCC CCA GAA ATA GTA GCT GGC TTG GAT GAG CTA GCT CTA GCA	2244
696	K T I R Y H P P E I V A G L D E L A L A	715
2245	ACT GAA CAT CTT GCC ATT GTG AAC CGA GCT TCG TGG GAT AGT TTC CTC AAG AGT TTC AGT	2304
716	T E H L A I V N R A S W D S F L K S F S	735
2305	AGA TAC TAC ACA GAT TTT AAG GCT GCC GTT CAA GCT CTT GCT GCA CTG GAC TGT TTG CAC	2364
736	R Y Y T D F K A A V Q A L A A L D C L H	755
2365	TCC CTT TCA ACT CTA TCT AGA AAC AAG AAC TAT GTG CGT CCC GAG TTT GTG GAT GAC TGT	2424
756	S L S T L S R N K N Y V R P E F V D D C	775

FIG.4D

2425	GAA CCA GTT GAG ATA AAC ATA CAG TCT GGT CGT CAT CCT GTA CTG GAG ACT ATA TTA CAA	2484
776	E P V E I N I Q S G R H P V L E T I L Q	795
2485	GAT AAC TTC GTC CCA AAT GAC ACA ATT TTG CAT GCA GAA GGG GAA TAT TGC CAA ATT ATC	2544
796	D N F V P N D T I L H A E G E Y C Q I I	815
2545	ACC GGA CCT AAC ATG GGA GGA AAG AGC TGC TAT ATC CGT CAA GTT GCT TTA ATT TCC ATA	2604
816	T G P N M G G K S C Y I R Q V A L I S I	835
2605	ATG GCT CAG GTT GGT TCC TTT GTA CCA GCG TCA TTC GCC AAG CTG CAC GTG CTT GAT GGT	2664
836	M A Q V G S F V P A S F A K L H V L D G	855
2665	GTT TTC ACT CGG ATG GGT GCT TCA GAC AGT ATC CAG CAT GGC AGA AGT ACC TTT CTA GAA	2724
856	V F T R M G A S D S I Q H G R S T F L E	875
2725	GAA TTA AGT GAA GCG TCA CAC ATA ATC AGA ACC TGT TCT TCT CGT TCG CTT GTT ATA TTA	2784
876	E L S E A S H I I R T C S S R S L V I L	985
2785	GAT GAG CTT GGA AGA GGC ACT AGC ACA CAC GAC GGT GTA GCC ATT GCC TAT GCA ACA TTA	2844
896	D E L G R G T S T H D G V A I A Y A T L	915
2845	CAG CAT CTC CTA GCA GAA AAG AGA TGT TTG GTT CTT TTT GTC ATG CAT TAC CCT GAA ATA	2904
916	Q H L L A E K R L V L F W T H Y P E I	935
2905	GCT GAG ATC AGT AAC GGA TTC CCA GGT TCT GTT GGG ACA TAC CAT GTC TCG TAT CTG ACA	2964
936	A E I S N G F P G S V G T Y H V S Y L T	955
2965	TTG CAG AAG GAT AAA GGC AGT TAT GAT CAT GAT GAT GTG ACC TAC CTA TAT AAG CTT GTG	3024
956	L Q K D K G S Y D H D D V T Y L Y K L V	975

FIG.4E

3025	CGT GGT CTT TGC AGC AGG AGC TTT GGT TTT AAG GTT GCT CAG CTT GCC CAG ATA CCT CCA	3084
976	R G L C S R S F G F K V A Q L A Q I P P	995
3085	TCA TGT ATA CGT CGA GCC ATT TCA ATG GCT GCA AAA TTG GAA GCT GAG GTA CGT GCA AGA	3144
996	S C I R R A I S M A A K L E A E V R A R	1015
3145	GAG AGA AAT ACA CGC ATG GGA GAA CCA GAA GGA CAT GAA GAA CCG AGA GGC GCA GAA GAA	3204
1016	E R N T R M G E P E G H E E P R G A E E	1035
3205	TCT ATT TCG GCT CTA GGT GAC TTG TTT GCA GAC CTG AAA TTT GCT CTC TCT GAA GAG GAC	3264
1036	S I S A L G D L F A D L K F A L S E E D	1055
3265	CCT TGG AAA GCA TTC GAG TTT TTA AAG CAT GCT TGG AAG ATT GCT GGC AAA ATC AGA CTA	3324
1056	P W K A F E F L K H A W K I A G K I R L	1075
3325	AAA CCA ACT TGT TCA TTT TGA TTAACTTAACATTATAGCACTGCAAGGCTTGATCACTGTTAGTTGCG	3397
1076	K P T C S F *	1082
3398	TACTACTT ATG TGT ATT AGT ATA ACA AGA AAA GAG AAT TAG AGAG ATG GAT TCT AAT CCG	3458
1	M C I S I T R K E N * M D S N P	5
3459	GTG TTG CAG TAC ATC TTT TCT CCA CCC GCA TAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3522
6	V L Q Y I F S P P A *	16

FIG.4F

MSH3-At --MGKK-----QQTISRFAPKPS-**THE**-PNPVAESSTPPK-----ISATVSFSPSKRLL
 MSH3-Sc MVIENEPLVLLRAKSSANRFILNLLTIMAGOPTISRFHKAVKSELTHKQEQEAVANGAGESICLDTDEEDNLSSVASTIVTNDSSFPLKGS
 MSH3-At SDHLAASP**KKPK**KLSPH**IQNP**VPDPNLHQ**PELQ**RLEP-----SPEEVPETSS...SRKYTPLEQ**QVVEL**KS**KYPD**VLMVE**VG**RYRF
 MSH3-Sc VSSKNSKSEKTS**GTST**IFNDIDFAKKLDRI**MKR**SDENVEAEDEEEGE**EDFV**KKKARKSP**TAKL**TP**LDKQ**VKD**LKMH**RD**KVL**IRV**G**YK**K**YK**K**
 MSH3-At FGEDAEIAAR**VLGI**YAH-----MDHN-----FMTAS**VP**TR**LN**F**HVR**RLV**NAGY**K**IGV**KOTET**IAIK**SH--GANRT**GP**FF**RGL**SAL**Y**TKA
 MSH3-Sc FAEDAVTSRIL**HLIK**LV**PGK**L**TID**ESNPQDC**NHQ**EAYCS**F**PDVRL**NVH**LER**LV**HN**LK**VAVEQ**AE**ISA**IKK**DPGASKSS**VFER**KIS**NV**FTKA
 MSH3-At ILEAE**DIS**GGCGGEE**GF**GSOS**NFL**VCVDERVKSET**L**GGGI**EMS**FDVR**VG**VE**IST**GE**VV**YEE**FND**-N**F**MRSG**EA**V**IL**SS**PA**ELL**LG**-Q**P**
 MSH3-Sc IFGVNSTFVLR-----GKR-----ILGDTNS**IWA**SRDV**HQ**GVAK**YSL**IS**NLN**NGEV**YD**EE**FP**N**LAD**E**KLQ**IR**IKY**L**Q**PIEV**LV**NT**DD**
 MSH3-At LSQ**TEK**FLV**AMAG**PT**SN**VRVERAS**LDC**FSNG**NA**DEV**IS**CEKIS**AG**NLEDD**KE**M**LEA**EKG**MS**CL**TV**HT**IM**N**PH**L**T**VO**AL**AL**TF**CH**LK**Q**FG**
 MSH3-Sc LPLHVAK**FE**K**DIS**CP**L**I**HQ**EYD**LED**H**VQ**AIK**WNE**K**IQ**L**SP**SL-----IRLVSKLYSHMVEYN
 MSH3-At FERIL**YQ**GA**SFR**SL**S**NT**EM**T**L**SANT**LQ**LEV**K**NSD**GES**GS**L**F**HN**M**HT**L**IV**GS**RL**LR**H**W**TH**PL**CD**R**N**L**IS**AR**LD**AV**SE**ISAC**MG**SHSS
 MSH3-Sc NEQ**VM**L**IP**SI**YSP**FA**SK**I**H**ML**LD**PN**S**LOS**L**D**IF**THD--G**GK**·G**SL**F**ML**LD**H**TRIS**FG**LR**ML**RE**W**IL**KP**L**V**D**V**HQ**IE**ER**LD**AE**IC**IT**SE**IN**NS**...
 MSH3-At QLSSELVEEGSERAI**VS**PEFY**LV**SS**VL**TAMSRSSD**IQ**R**GI**TR**I**F**H**RI**AK**ATE**FI**AV**ME**AIL**LAG**Q**IQ**RL**GI**KOD**SE**MR**S**MQ**S**-AT**VR**ST**IL**LR**K**
 MSH3-Sc -----IFFES**L**NQ**ML**N**HT**PD**LL**RT**LN**R**IM**GY**ITS**RKE**IV**FY**LK**Q**ITS**FVD**HF**K**HQ**S**YL**SE**HF**KSSD**GR**IG**KQ**SP**LL**FR
 MSH3-At LIS**VI**SS**PV**V**VD**N**AG**KL**S**AL**NKE**A**AV**RG---DLL**D**IL**ITS**-SD**Q**PE**LA**E**ARQ**AV**LI**RE**K**LDSS**IAS**FR**KK**L**AI**R**N**LE**FL**Q**VS**GI**TH**L**IEL**P
 MSH3-Sc L**FS**EL**N**ELL**ST**Q**L**PH**FL**TM**IN**VS**AV**MEK**NSD**KQ**VM**DF**FN**LN**NY**DC**SE**GI**IK**IQ**RE**SE**S**VR**SQ**L**KE**EL**AE**IR**K**YL**K**RP**YL**NE**RF**DEV**D**YL**IE**V**K**NS

FIG. 5A

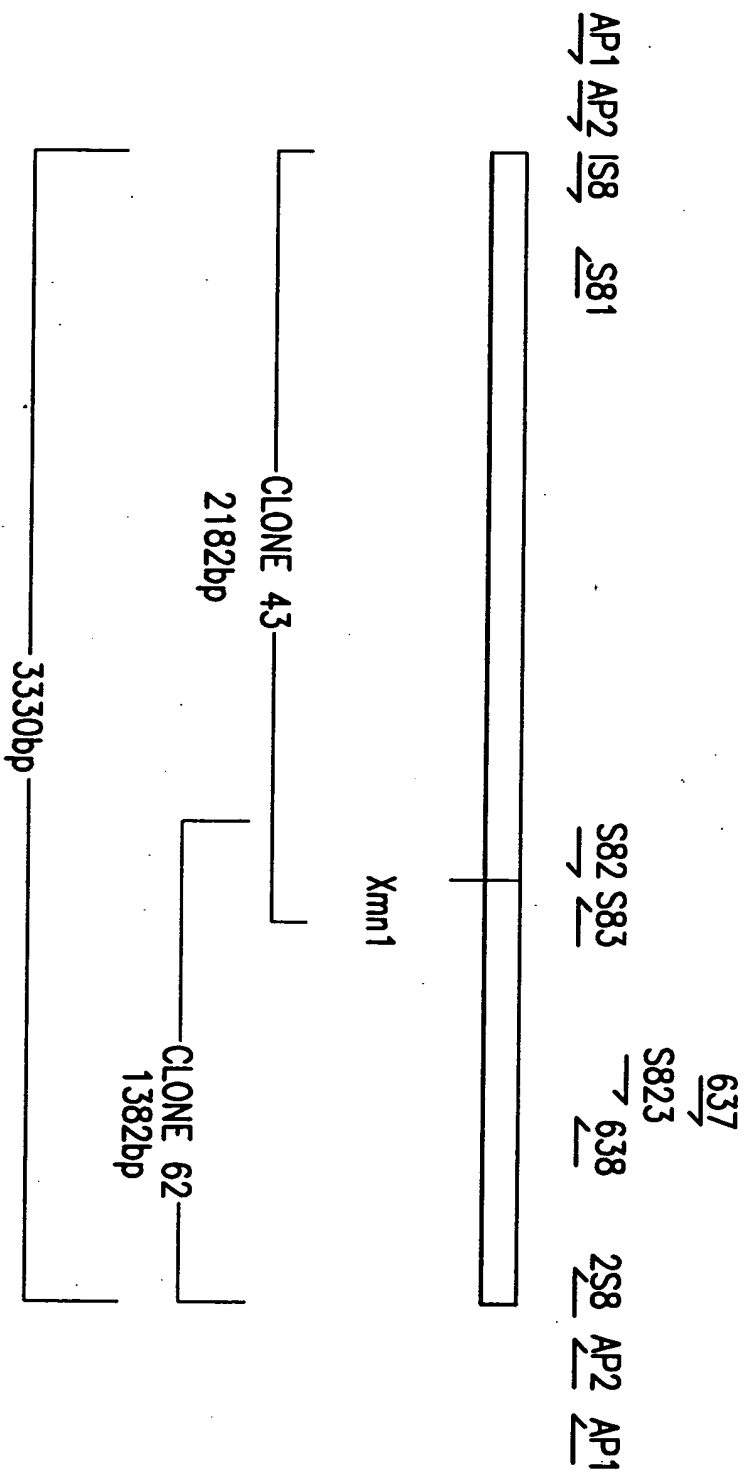
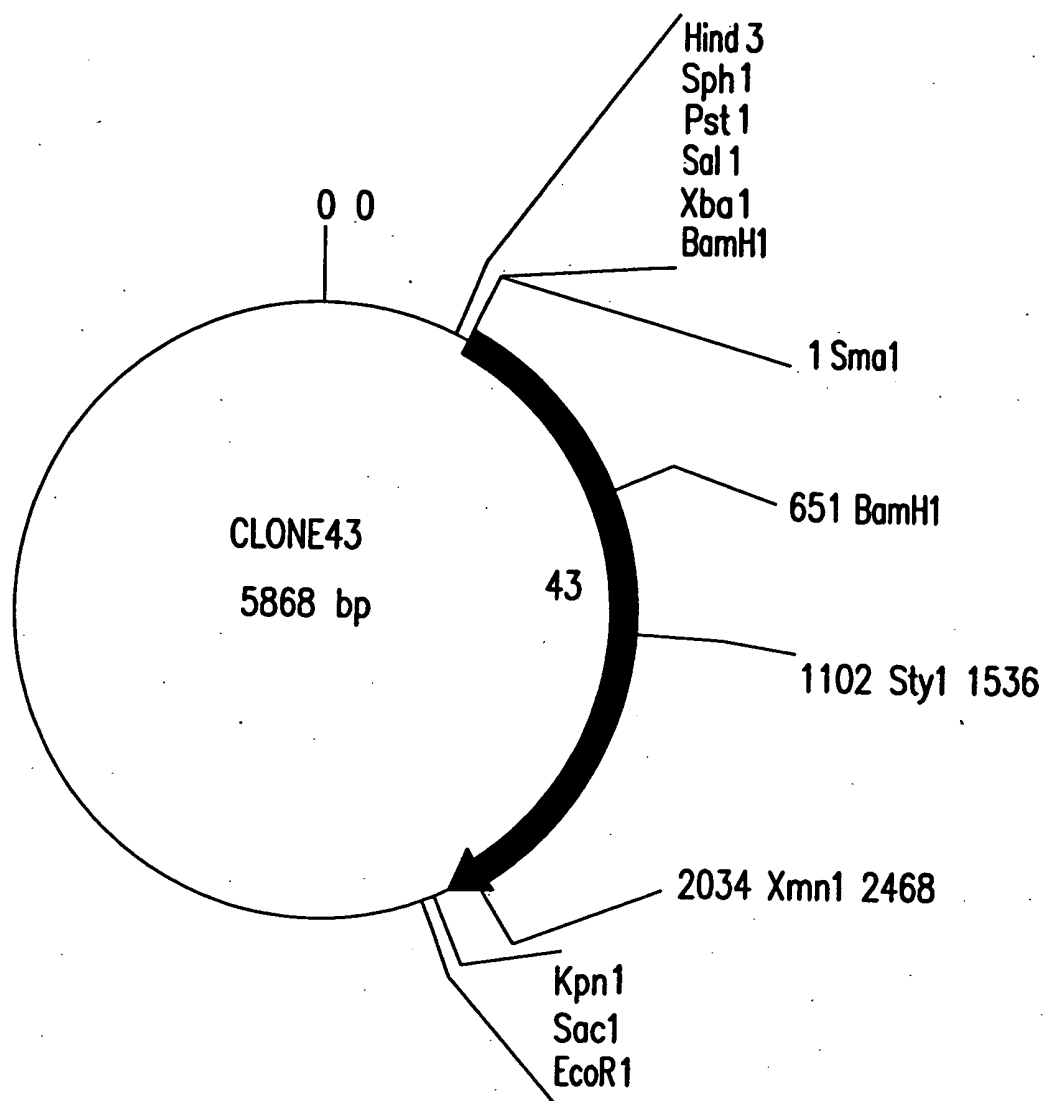
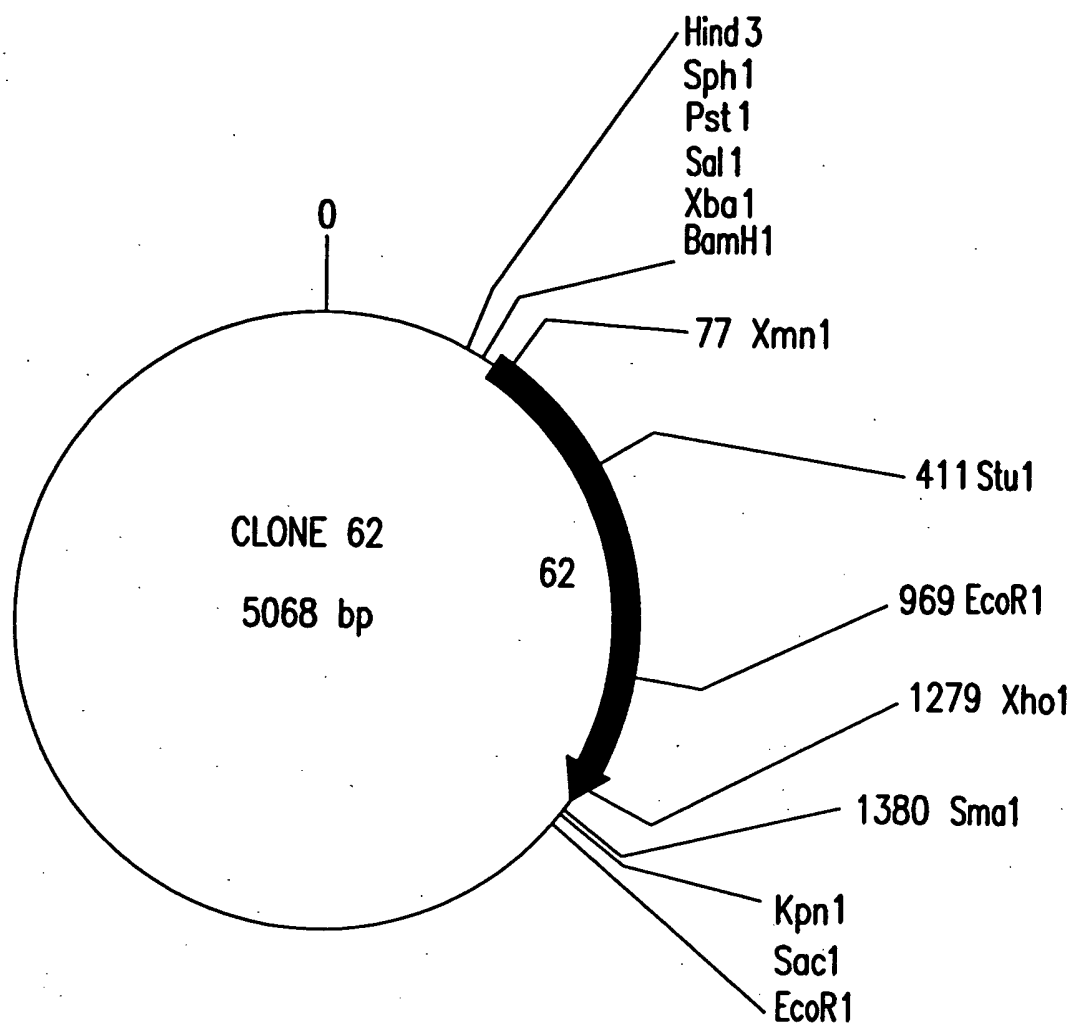


FIG. 6



COMMENTS/REFERENCES: 43=5' SIDE OF S8 (AtMSH6) 2182bp IN pUC18/Sma1

FIG.7



COMMENTS/REFERENCES: 62=3' SIDE OF S8 (AtMSH6) 1379bp IN pUC18/Sma1

FIG.8

694	TCT CGC TTG AAG CGA GTT CTG GAG GAT GAA ATG ACT TTT AAG GAG GAT AAG GTT CCT GTA	753
185	S R L K R V L E D E M T F K E D K V P V	204
754	TTG GAC TCT AAC AAA AGG CTG AAA ATG CTC CAG GAT CCG GTT TGT GGA GAG AAG AAA GAA	813
205	L D S N K R L K M L Q D P V C G E K K E	224
814	GTA AAC GAA GGA ACC AAA TTT GAA TGG CTT GAG TCT TCT CGA ATC AGG GAT GCC AAT AGA	873
225	V N E G T K F E W L E S S R I R D A N R	224
874	AGA CGT CCT GAT GAT CCC CTT TAC GAT AGA AAG ACC TTA CAC ATA CCA CCT GAT GTT TTC	933
245	R R P D D P L Y D R K T L H I P P D V F	264
934	AAG AAA ATG TCT GCA TCA CAA AAG CAA TAT TGG AGT GTT AAG AGT GAA TAT ATG GAC ATT	993
265	K K M S A S Q K Q Y W S V K S E Y M D I	284
996	GTG CTT TTC TTT AAA GTG GGG AAA TTT TAT GAG CTG TAT GAG CTA GAT GCG GAA TTA GGT	1053
285	V L F F K V G K F Y E L Y E L D A E L G	304
1054	CAC AAG GAG CTT GAC TGG AAG ATG ACC ATG AGT GGT GTG GGA AAA TGC AGA CAG GTT GGT	1113
305	H K E L D W K M T M S G V G K C R Q V G	324
1114	ATC TCT GAA AGT GGG ATA GAT GAG GCA GTG CAA AAG CTA TTA GCT CGT GGA TAT AAA GTT	1173
325	I S E S G I D E A V Q K L L A R G Y K V	344
1174	GGA CGA ATC GAG CAG CTA GAA ACA TCT GAC CAA GCA AAA GCC AGA GGT GCT AAT ACT ATA	1233
345	G R I E Q L E T S D Q A K A R G A N T I	364
1234	ATT CCA AGG AAG CTA GTT CAG GTA TTA ACT CCA TCA ACA GCA AGC GAG GGA AAC ATC GGG	1293
365	I P R K L V Q V L T P S T A S E G N I G	384
1294	CCT GAT GCC GTC CAT CTT CTT GCT ATA AAA GAG ATC AAA ATG GAG CTA CAA AAG TGT TCA	1353
385	P D A V H L L A I K E I K M E L Q K C S	404

FIG.9B

1354	ACT GTG TAT GGA TTT GCT TTT GTT GAC TGT GCT GCC TTG AGG TTT TGG GTT GGG TCC ATC	1413
405	T V Y G F A F V D C A A L R F W V G S I	424
1414	AGC GAT GAT GCA TCA TGT GCT GCT CTT GGA GCG TTA TTG ATG CAG GTT TCT CCA AAG GAA	1473
425	S D D A S C A A L G A L L M Q V S P K E	444
1474	GTG TTA TAT GAC AGT AAA GGG CTA TCA AGA GAA GCA CAA AAG GCT CTA AGG AAA TAT ACG	1533
445	V L Y D S K G L S R E A Q K A L R K Y T	464
1534	TTG ACA GGG TCT ACG GCG GTA CAG TTG GCT CCA GTA CCA CAA GTA ATG GGG GAT ACA GAT	1593
465	L T G S T A V Q L A P V P Q V M G D T D	484
1594	GCT GCT GGA GTT AGA AAT ATA ATA GAA TCT AAC GGA TAC TTT AAA GGT TCT TCT GAA TCA	1653
485	A A G V R N I I E S N G Y F K G S S E S	504
1654	TGG AAC TGT GCT GTT GAT GGT CTA AAT GAA TGT GAT GTT GCC CTT AGT GCT CTT GGA GAG	1713
505	W N C A V D G L N E C D V A L S A L G E	524
1714	CTA ATT AAT CAT CTG TCT AGG CTA AAG CTA GAA GAT GTA CTT AAG CAT GGG GAT ATT TTT	1773
525	L I N H L S R L K L E D V L K H G D I F	544
1774	CCA TAC CAA GTT TAC AGG GGT TGT CTC AGA ATT GAT GGC CAG ACG ATG GTA AAT CTT GAG	1833
545	P Y Q V Y R G C L R I D G Q T M V N L E	564
1834	ATA TTT AAC AAT AGG TGT GAT GGT GGT CCT TCA GGG ACC TTG TAC AAA TAT CTT GAT AAC	1893
565	I F N N S C D G G P S G T L Y K Y L D N	584
1894	TGT GTT AGT CCA ACT GGT AAG CGA CTC TTA AGG AAT TGG ATC TGC CAT CCA CTC AAA GAT	1953
585	C V S P T G K R L L R N W I C H P L K D	604
1954	GTA GAA AGC ATC AAT AAA CGG CTT GAT GTA GTT GAA GAA TTC ACG GCA AAC TCA GAA AGT	2013
605	V E S I N K R L D V V E E F T A N S E S	624

FIG.9C

2014	ATG CAA ATC ACT GGC CAG TAT CTC CAC AAA CTT CCA GAC TTA GAA AGA CTG CTC GGA CGC	2073
625	M Q I T G Q Y L H K L P D L E R L L G R	644
2074	ATC AAG TCT AGC GTT CGA TCA TCA GCC TCT GTG TTG CCT GCT CTT CTG GGG AAA AAA GTG	2133
645	I K S S V R S S A S V L P A L L G K K V	664
2134	CTG AAA CAA CGA GTT AAA GCA TTT GGG CAA ATT GTG AAA GGG TTC AGA AGT GGA ATT GAT	2193
665	L K Q R V K A F G Q I V K G F R S G I D	684
2194	CTG TTG TTG GCT CTA CAG AAG GAA TCA AAT ATG ATG AGT TTG CTT TAT AAA CTC TGT AAA	2253
685	L L L A L Q K E S N M M S L L Y K L C K	704
2254	CTT CCT ATA TTA GTA GGA AAA AGC GGG CTA GAG TTA TTT CTT TCT CAA TTC GAA GCA GCC	2313
705	L P I L V G K S G L E L F L S Q F E A A	724
2314	ATA GAT AGC GAC TTT CCA AAT TAT CAG AAC CAA GAT GTG ACA GAT GAA AAC GCT GAA ACT	2373
725	I D S D F P N Y Q N Q D V T D E N A E T	744
2374	CTC ACA ATA CTT ATC GAA CTT TTT ATC GAA AGA GCA ACT CAA TGG TCT GAG GTC ATT CAC	2433
745	L T I L I E L F I E R A T Q W S E V I H	764
2434	ACC ATA AGC TGC CTA GAT GTC CTG AGA TCT TTT GCA ATC GCA GCA AGT CTC TCT GCT GGA	2493
765	T I S C L D V L R S F A I A A S L S A G	784
2494	AGC ATG GCC AGG CCT GTT ATT TTT CCC GAA TCA GAA GCT ACA GAT CAG AAT CAG AAA ACA	2553
785	S M A R P V I I F P E S E A T D Q N Q K T	804
2554	AAA GGG CCA ATA CTT AAA ATC CAA GGA CTA TGG CAT CCA TTT GCA GTT GCA GCC GAT GGT	2613
805	K G P I L K I Q G L W H P F A V A A D G	824
2614	CAA TTG CCT GTT CCG AAT GAT ATA CTC CTT GGC GAG GCT AGA AGA AGC AGT GGC AGC ATT	2673
825	Q L P P V P N D I L L G E A R R S S G S I	844

FIG.9D

2674	CAT CCT CGG TCA TTG TTA CTG ACG GGA CCA AAC ATG GGC GGA AAA TCA ACT CTT CTT CGT	2733
845	H P R S L L L T G P N M G G K S T L L R	864
2734	GCA ACA TGT CTG GCC GTT ATC TTT GCC CAA CTT GGC TGC TAC GTG CCG TGT GAG TCT TGC	2793
865	A T C L A V I F A Q L G C Y V P C E S C	884
2794	GAA ATC TCC CTC GTG GAT ACT ATC TTC ACA AGG CTT GGC GCA TCT GAT AGA ATC ATG ACA	2853
885	E I S L V D T I F T R L G A S D R I M T	904
2854	GGA GAG AGT ACC TTT TTG GTA GAA TGC ACT GAG ACA GCG TCA GTT CTT CAG AAT GCA ACT	2913
905	G E S T F L V E C T E T A S V L Q N A T	924
2914	CAG GAT TCA CTA GTA ATC CTT GAC GAA CTG GGC AGA GGA ACT AGT ACT TTC GAT GGA TAC	2973
925	Q D S L V I L D E L G R G T S T F D G Y	944
2974	GCC ATT GCA TAC TCG GTT TTT CGT CAC CTG GTA GAG AAA GTT CAA TGT CGG ATG CTC TTT	3033
945	A I A Y S V F R H L V E K V Q C R M L F	964
3034	GCA ACA CAT TAC CAC CCT CTC ACC AAG GAA TTC GCG TCT CAC CCA CGT GTC ACC TCG AAA	3093
965	A T H Y H P L T K E F A S H P R V T S K	984
3094	CAC ATG GCT TGC GCA TTC AAA TCA AGA TCT GAT TAT CAA CCA CGT GGT TGT GAT CAA GAC	3153
985	H M A C A F K S R S D Y Q P R G C D Q D	1004
3154	CTA GTG TTC TTG TAC CGT TTA ACC GAG GGA GCT TGT CCT GAG AGC TAC GGA CTT CAA GTG	3213
1005	L V F L Y R L T E G A C P E S Y G L Q V	1024
3214	GCA CTC ATG GCT GGA ATA CCA AAC CAA GTG GTT GAA ACA GCA TCA GGT GCT GCT CAA GCC	3273
1025	A L M A G I P N Q V V E T A S G A Q A	1044
3274	ATG AAG AGA TCA ATT GGG GGA AAC TTC AAG TCA AGT GAG CTA AGA TCT GAG TTC TCA AGT	3333
1045	M K R S I G E N F K S S E L R S E F S S	1064

FIG.9E

3334	CTG CAT GAA GAC TGG CTC AAG TCA TTG GTG GGT ATT TCT CGA GTC GCC CAC AAC AAT GCC	3393
1065	L H E D W L K S L V G I S R V A H N N A	1084
3394	CCC ATT GGC GAA GAT GAC TAC GAC ACT TTG TTT TGC TTA TGG CAT GAG ATC AAA TCC TCT	3453
1085	P I G E D D Y D T L F C L W H E I K S S	1104
3454	TAC TGT GTT CCC AAA TAA ATG GCT ATG ACA TAA CACTAICTGAAGCTCGTTAAGTCCTTGCCCTCT	3521
1105	Y C V P K * M A M T *	5
3522	G ATG TTT ATT CCT CTT AAA AAA TGC TTA TAT ATC AAA AAA TTG TTT CCT CGA TTA AAA	3579
1	M F I P L K K C L Y I K K L F P R L K	19
3580	AAA AAA AAA AAA AAA AAA AAA AAA	3606
20	K K K K K K K K	28

FIG.9F

AtMSH6-mi
MSH6_yeast
-----MQR---QRSL~~STFF~~-----QKPTAATIKGLVSGDAASGG-~~GGSGGPRFNVREGDAKGDAVFAVSKSVDEVRGDT~~
MAPATPKSTIAHFENGSTSSQKKMKQSSLSFSKQVPSGTPSKKVIQKPTPATIENTATDKITKNPQGGKIGL~~FVDVDEDND-LITAEETVSVTRSDIMHSQE~~

AtMSH6-mi
MSH6_yeast
~~PPEKVP~~RRVLPSGFK~~PAESAGDASSLFSNIMHK~~---FVKVDDRD---CSGERSREDVPLN-DSSLCKMANDVIPQFRSNNGKTIERNHAFSFSG-RAELRS
POSDTMLNSNTTEPKSTTTDEDLSSSQSRNHKRRVVAESDDDDSDITFTAKRKKGKIVDSESEDEDEYLPDKNDGDEDDIADDKEDIK~~GELAE~~DSGDDDDLIS

AtMSH6-mi
MSH6_yeast
VEDIGVDGVPGETPGMRPRASRLKRVLEDEMTFEKEDV~~PVLD~~SNKRLKMLQDPVCGEKEKEVNEGTFEWL~~ESSRI~~RDANRRRPDDPL~~YDRK~~TLHIP~~PDVFK~~KN
LAETTSKKKFSYNTSHSSSPFTRNISRDNSSKKSRPNQAPSRSYNP~~SHSQPSATS~~SSK~~FNK~~ONEERYQMLVDE--RDAQRRPKSDPEYDPRTILVIPSSAWNKF

AtMSH6-mi
MSH6_yeast
SASQKQYMSVKSEYMDIVLFEKVGKFEYEL~~DAELGH~~KELD~~MDQMT~~SGV~~GKCR~~QVGI~~SES~~GIDEAVQKLLAR~~GYKVGRI~~EQLETSDQAKAR-GANTIIIPRKLIVQ
TPFEKQYWEIKSKMDCIVFEKKKGKFEYEL~~DAELGH~~KELD~~MDQMT~~SGV~~GKCR~~QVGI~~SES~~GIDEAVQKLLAR~~GYKVGRI~~EQLETSDQAKAR-GANTIIIPRKLIVQ

AtMSH6-mi
MSH6_yeast
VLTPSIASEGNIGP--DAVHL~~LAIKE~~-----IKMELQKS--..-TVYGFAFVDCALRFWVGSISDDASGALGAILMOVSPKEVL~~YDSKGLS~~REAQKALR
ILISGLITDGDMLHSDLAITFC~~LAI~~REEPGNFVNETQLDSSITIVQKLN~~TKIFGA~~FIDITATGELQMLEFEDDSEGT~~IKLDTLMSQVRPMEV~~MERNMLSTLANKIVK

AtMSH6-mi
MSH6_yeast
KYTLTGSTAVQLAPVPQVMGDTDAAGVRNII~~IESNGYFKGSS~~ES~~WNC~~AVDGLNEC--DVALSALGEL~~LNHLSR~~KELED--VLKHGDI~~F~~PYQVYRGCLRIDGQITMV
FNSAPMAIFNEVKAGEEFY---DCDKTYAEIIISSEYFS TEEDWPEVLKSYDTGKKVGFSAFGCLLYVLKMLKLDKNLISMKNIKEYDFVKSQHSWLDGITLQ

AtMSH6-mi
MSH6_yeast
~~NLEIFENNS~~CDGSPSGITLYKVL~~DNCVSPTGKRLRN~~WICHPLKDVES~~INKRLDV~~EEFTANSESMTGQYLHKL~~PDLERLLGR~~IKS.....
~~NLEIFSNS~~FDGSDKGTILFKL~~FNRAITTPGKRMWK~~MLMPLLRKND~~IESRLDS~~VDSLQDITLREQLEITFSKLP~~LERMLARI~~HSRTIKVKDFEKVITAFETII

AtMSH6-mi
MSH6_yeast
-----SVRSS-----ASVLPALLGKKVLKQ~~RVKAF~~GQIVKGRSGIDILLALQKE-----SNMMSLLYKLC~~KLPILV~~GKSGLELFLSQFEAA
ELQDSLKNNDLKG~~DVSKYISSF~~PEGLVE~~AVK~~SWTNAFEROKAINENIIVPQ~~RGFDIE~~FDKSM~~DRIQ~~ELEDELMEILMTYRKQFKCSN~~IQYKDSGKEI~~YITIEIPIS

AtMSH6-mi
MSH6_yeast
IDSDFPN-----YQND-----VTDENAEITLILIELFIERATQ-----WSEVHTSTICLDMLRSFAIASLSAGSMARVIFPES~~EATDQ~~N
ATKNVPSNWVQMAANKTYKRYVSE~~VRALAR~~SM~~AEAKEI~~HKTLLEEDLKNRLCQKFD~~AHNTIIMPT~~IOAISNIDCLLAITRITSEYLGAPSCGRPTIVDEVDSKTN

FIG.10A

AtMSH6-mi	QKTKGPI LKIQGLWHPFA--VAADGQLPVPNDILLGEARRSSGSIHPRSLLTGPNMGKSTILLRATQLAVTFADLGCYVPCESCEISLVDITIFTRLGASDRIMT
MSH6_yeast	QLNG--FLKFKSLRHPCFNLGATTAKDFIPNDIELKEQ-----PRLGLTGAMAGKSTILRMAGIAVIMAGMGCYVPCESAVLTPIDRIMTRLGANDNIMQ
AtMSH6-mi	GESTTELVECTETIASVLDNATQDSLVILDELGRGISTFDGYAIAYSVFRHLVEKVQCRMLEATHYHPLTKEEASHPRVITSKHMACAFKSRSDYQPRGCDQDLVFLY
MSH6_yeast	GKSTFFVELAETIKKILDMATNRSLLVDELGRGSSDGFATIAESVLHVATHIQSLGFFATHYGTILASSFKHHPOVRPLKMSILVDEAT-----RNVTFLY
AtMSH6-mi	RLTEGACPESYGLQVALMAGIPNQVETASGAQ-----AMKRSIGENFKSSSLRSEFSSLHEDMLKSLVGISRVAHNNAPIGE----DDYDTLFCFLWHEIK
MSH6_yeast	KMLEGQSEGSFEGMHVASMCGISKEIIDNAQIAADNLEHTSRLVKERDLAANNLNGEIVSVPGGLQSDFVR IAYGDG-LKNTKLGSGEGLNYPDNIKRNVLKSLF
AtMSH6-mi	SSYCVPK-
MSH6_yeast	SIIDDLQS

FIG.10B

TTTTTTGGTTGCTAACAAATAAAGGTATACGGTTTTATGTCATCAATATAA	50
CTATATATAAAAGAAATGAAAGATATATATTGTTTTTTCATTTATCAAAC	100
AAAACAACAAGACTTTTTTTTTTACTTTTTACATTGGTCAACAAAATACAA	150
GATAAACGACATCGTTTAATCATTTTCCCAATTTTACCCCTAAGTTTAACA	200
CCTAGAACCTTCTCCATCTTCGCAAGCACAGCCTGATTAGGAACAGCTTT	250
ACCATTCATATTCTGAACTACCTGAGTCCTCTCATTGATCTGTTTCG	300
CCAAATCCGCTTGTGACATCTTCTTCTCCAATCTCGCTTCTGTATCATC	350
AACCTCACCTCTGCTTTCACACGATCCATCGCCGCAGGCTCTGTTTCTTC	400
TTCCAGCTTCTTCGTGTTAATCACCGGAACCGCCGTAGATTTCCCCTTTT	450
TGTTCGAACC GG CATCGAATTTCTTAACCGTTTGAACCGCGACACCGTTT	500
CTCAGAGCTGCGTTAACCGCTTTCGGATCGCGTAGGCTTGGCTCTTTTG	550
TTTTGATTTGTGGAGAACTACTGGTTC C CAGTCTTGTGTTACTGCTCCTG	600
GGTATCTGCTCGGCATCGTCGATGAATTGAGAGAAAGGAACAACGCGAAA	650
ATTTTATTAATCTGAGTTTTGAAATTGAGAAACGATGAAGATGAAGAATG	700
TTGTTGAGAGGATTGTGATATTTATATACGAAGATTGGTTTCTGGAGA	750
ATTGATCATCTTTTTCTCCATTTTCGTCTCTGGAACGTTCTTAGAGATG	800
ATTGACGACGTGTCATTATCTGATTTGCAGTTAACCAATGCTTTTTGGGT	850
TGGATTCGTGGTACACCATATTATCCGATTTGGCTCAATGGTTTTATATA	900
AATTTGGTTTTTCGGTTTCGGTTATGAGTTATCATTAAAAATTAAGCTAACCA	950
AAAATTTTCGTAAAATTTATTTTCGGTTTCAATTCGGATCCCTTACTTCCA	1000
GAACCGAATTATTCGAAACCGGGTTAGCCGAACCGAATACCAATGCCTG	1050
ATTGACTCGTTGGCTAGAAAGATCCAACGGTATACAATAATAGAACATAA	1100
ATCGGACGGTCATCAAAGCCTCAAAGAGTGAACAGTCAACAAAAAAGTT	1150
GAGCCCTGAGGAGTATCGTTTTCCGCCATTTCTACGACGCAAGGCGAAAAT	1200
TTTTGGCGCAATCTTTCCCCCTTTCGAATTCTCTCAGCTCAAAACATC	1250
GTTTCTCTCTCACTCTCTCTCACAAATTCAAAAAATGCAGCGCCAGAGAT	1300
CGATTTTGTCTTTCTTCCAAAAACCCACGGCGGCGACTACGAAGGGTTTG	1350
GTTTCCGGCGATGCTGCTAGCGGCGGGGGCGGCAGCGGAGACCACGATTT	1400
AATGTGAAGGAAGGGGATGCTAAAGGCGACGCTTCTGTACGTTTTGTGT	1450
TTCGAAATCTGTGATGAGGTTAGAGGAACGGATACTCCACCGGAGAAGG	1500
TTCCGCGTCGTGTCCTGCCGTCTGGATTTAAGCCGGCTGAATCCGCCGGT	1550
GATGCTTCGTCCCTGTTCTCCAATATTATGCATAAGTTTGTAAAAGTCGA	1600
TGATCGAGATTGTTCTGGAGAGAGGTAATACTTCGATTCTCTTAATTT	1650
TGTTATCTTTAGCTGGAAGAAGAAGATTCGTGTAATTTGTTGTATTCTGT	1700
GGAGAGATTCTGATTACTGCATTGGATCGTTGTTTACAAATTTTCAGGAG	1750
CCGAGAAGATGTTGTTCCGCTGAATGATTCATCTCTATGTATGAAGGCTA	1800
ATGATGTTATTCCTCAATTTCTGTTCCAATAATGGTAAAACTCAAGAAAGA	1850
AACCATGCTTTTAGTTTCAGTGGGAGAGCTGAACTTAGATCAGTAGAAGA	1900
TATAGGAGTAGATGGCGATGTTCTGTGTCAGAAACACCAGGGATGCGTC	1950
CACGTGCTTCTCGCTTGAAGCGAGTTCTGGAGGATGAAATGACTTTTAAG	2000
GAGGATAAGGTTCTGTATTGGACTCTAACAAAAGGCTGAAAATGCTCCA	2050

FIG. 11A

GGATCCGGTTTGTGGAGAGAAGAAAGAAGTAAACGAAGGAACCAAATTTG	2100
AATGGCTTGAGTCTTCTCGAATCAGGGATGCCAATAGAAGACGTCCTGAT	2150
GATCCCCTTTACGATAGAAAGACCTTACACATACCACCTGATGTTTTCAA	2200
GAAAATGTCTGCATCACAAAAGCAATATTGGAGTGTTAAGAGTGAATATA	2250
TGGACATTGTGCTTTTCTTTAAAGTGGTTAGTAACTATTAATCTAGTGTT	2300
CAATCCATTTCTCAATGTGATTTGTTCACTTACATCTGTTTACGTTATG	2350
CTCTTCTCAGGGGAAATTTTATGAGCTGTATGAGCTAGATGCGGAATTAG	2400
GTCACAAGGAGCTTGACTGGAAGATGACCATGAGTGGTGTGGGAAAATGC	2450
AGACAGGTAAATTAGTTGAAACAACCTGGCCTGCTTGAATTATTGTGTCTA	2500
TAAATTTTGACACCACCTTTTGTTCAGGTTGGTATCTCTGAAAGTGGGA	2550
TAGATGAGGCAGTGCAAAAGCTATTAGCTCGTGGGTAAGGGAACCATCAT	2600
ACTTTATGGAATTCGTTTACTGCTACTTCGGCTAGGATTTAAGAAATGGA	2650
AATCACTTCAAGCATCATTAGTTAGGATCCTGAGAACTCAGGATGTTTTCT	2700
TTATTCGTTATATAATAAGTCTTTTCATCAAGGAGTAACAAACAAAACCT	2750
GCACAATATTTGTGTGCTCACTGGCAAGGCATATATACCCAGCTAACCTT	2800
TGCTAGTTCAGTGTAGTAACAGTTACGGATAATATATGTTTACTTGTATG	2850
TGGTACCCTCATTTTGTCTCTCATGGAGGCTTCAAGCCTTGTGTTGAAA	2900
CTGGATAGTTACATATGCTTCCAACAGAACTAGCATGCAGATTCATATG	2950
CTTTCCTATTCTACTAATTATGTATTGACACACTCGTTGTTTCTTTTGAA	3000
AGATATAAAGTTGGACGAATCGAGCAGCTAGAAACATCTGACCAAGCAAA	3050
AGCCAGAGGTGCTAATACTGTAAGTTTTCTTGGATAGGTCAAGGAGAGTG	3100
TTGCAGACTGTTTTTGATCATTTTCTTTTCTGTACATTACTTTCATGCTG	3150
TAATTAACCTAATGGCTATTCTGGTCTGATTATCAGATAATTCCAAGGAA	3200
GCTAGTTCAGGTATTAACCTCATCAACAGCAAGCGAGGGAAACATCGGGC	3250
CTGATGCCGTCCATCTTCTTGCTATAAAAGAGGTTTGTTATTTACTTATT	3300
TATCTTATCATGTTCAAGTTCATCCAAGTCCTGAAAAATTACACTCTTCTT	3350
TACCAATCTTCCATCAAGCTGTGTAAAGGATTTGGAATTAGAAAATCATT	3400
ATTTGATGCTTTGTTTTATATGCAAGAGGTTCCCTTGAAAAGATCTGTTT	3450
AAGATTCTTTGCACTTGAAAAATTCAATCTTTTAAAGTGAATCCCCTACT	3500
TTCTTACAATGATCATAGTCTGCAATTGCATGTCAAGTAATATCATTCTT	3550
TGTTACTGCATCCCCCTCTTCTTAATGACCATTGTCTATGTTGTGTTTG	3600
TCTCGTGTGCTGGAGAAAATGATAGCTGATCCAAGCTGTACATTATCATG	3650
ATTAAGTAGCTGCTCAGGAATTGCCTTTGGTTACATTGCCTAATGGTTTG	3700
ATGTCAATTTTTCTTCTGAATCTTTATTTTAGATCAAAATGGAGCTACAA	3750
AAGTGTTCAACTGTGTATGGATTTGCTTTTGTTGACTGTGCTGCCTTGAG	3800
GTTTTGGGTTGGGTCCATCAGCGATGATGCATCATGTGCTGCTCTTGGAG	3850
CGTTATTGATGCAGGTAAGCAAGTGATTCTGTATCTTATGTGTACCATG	3900
TGACTTCCTGTGCATATATTTGGGTTGCAGGAACTAATTCTGAATCACCA	3950
TTTGGTATGTTTTTTCCAGGTTTCTCCAAAGGAAGTGTTATATGACAGTA	4000
AAGGTAACTGCTTGTATCGCCAGTTGTTTTGTAAACAGAATTTAAGGT	4050
AAATGACACTGGTTAATTTAAAGTGCATACATGTTGAAATATTGCAGGGC	4100

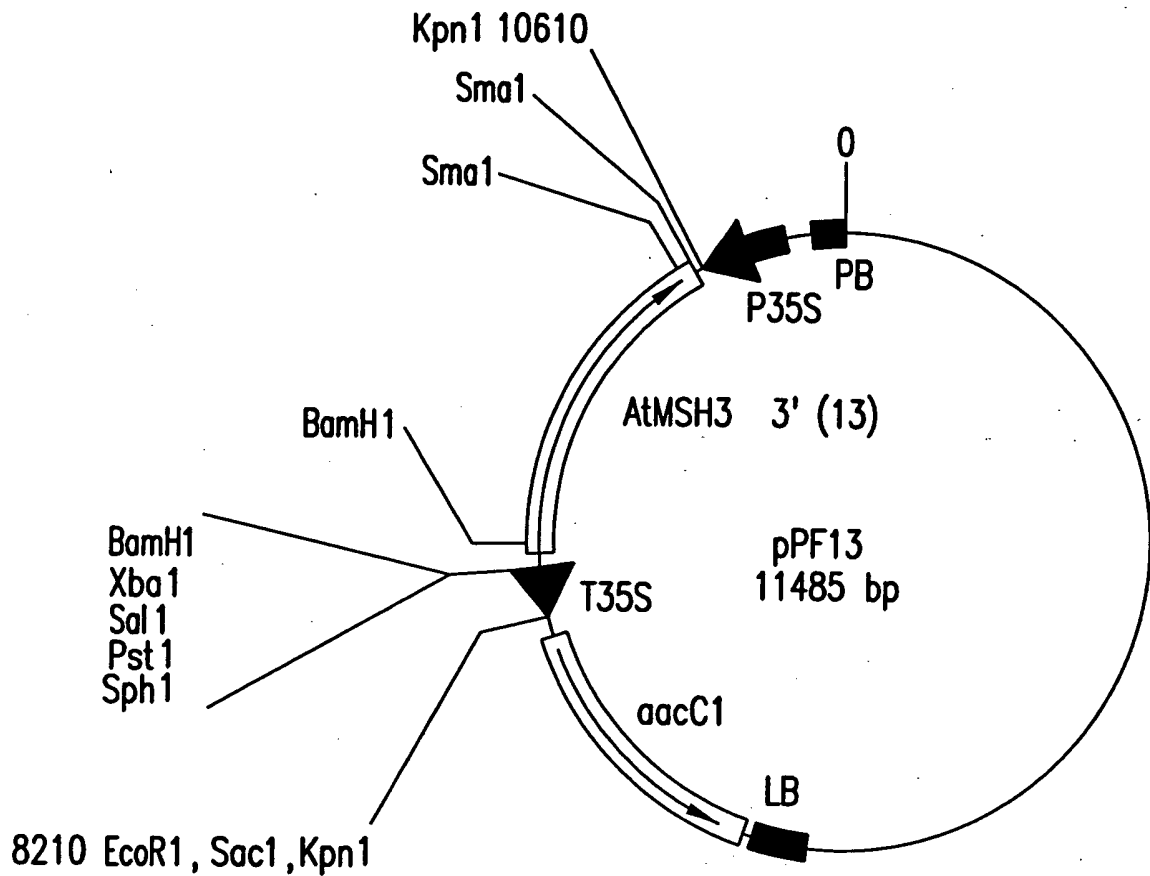
FIG. 11B

TATCAAGAGAAGCACAAAAGGCTCTAAGGAAATATACGTTGACAGGTACC	4150
ATTTCAAGTAGGCAAGCTAACTGACAATTTAACCGCTCACCGAATGATAGG	4200
TCTCTTAAACATTGCTAATGTAGATGATGTTTATGTTTCAATCTAATAGG	4250
GTCTACGGCGGTACAGTTGGCTCCAGTACCACAAGTAATGGGGGATACAG	4300
ATGCTGCTGGAGTTAGAAATATAATAGAATCTAACGGATACTTTAAAGGT	4350
TCTTCTGAATCATGGAAGTGTGCTGTTGATGGTCTAAATGAATGTGATGT	4400
TGCCCTTAGTGCTCTTGGAGAGCTAATTAATCATCTGTCTAGGCTAAAGG	4450
TGTGTTGGCTTGTTTAGTTTTTGCTTTTCACAAATTAAGCAAAGGAAGTT	4500
TTCACTAAGTACAGTTTCTATCTACTTGCAGCTAGAAGATGTACTTAAGC	4550
ATGGGGATATTTTCCATACCAAGTTTACAGGGGTTGTCTCAGAATTGAT	4600
GGCCAGACGATGGTAAATCTTGAGATATTTAACAATAGCTGTGATGGTGG	4650
TCCTTCAGGCAAGTGCATATTTCTTTTTTGATAACTTCACTAGAGGGCA	4700
GACATAGAAGGAAAAATTCTAATACTTCGTACGGATCTCCAGTAAGTAAT	4750
AGCCGATTTTTGTTTACCTATGTAGGGACCTTGACAAATATCTTGATAA	4800
CTGTGTTAGTCCAAGTGGTAAGCGACTCTTAAGGAATTGGATCTGCCATC	4850
CACTCAAAGATGTAGAAAGCATCAATAAACGGCTTGATGTAGTTGAAGAA	4900
TTACAGGCAAACTCAGAAAGTATGCAAATCACTGGCCAGTATCTCCACAA	4950
ACTTCCAGACTTAGAAAGACTGCTCGGACGCATCAAGTCTAGCGTTGAT	5000
CATCAGCCTCTGTGTTGCTGCTCTTCTGGGGAAAAAGTGTGAAACAA	5050
CGAGTAAGTATCAATCACAAGTTTTCTGAGTAATGCCTTCCATGAGTAGT	5100
ATAGGACTAAACATTACGGGTCTAGCTAAAGACTGTTCTCCTTCTTTTG	5150
CAATGTCTGGTTATTCATTACATTTCTCTTAAGTATTGCATTGCAGGTT	5200
AAAGCATTGTTGGCAAATTGTGAAAGGGTTCAGAAGTGAATTGATCTGTT	5250
GTTGGCTCTACAGAAGGAATCAAATATGATGAGTTTGCTTTATAAACTCT	5300
GTAAACTTCCTATATTAGTAGGAAAAAGCGGGCTAGAGTTATTTCTTTCT	5350
CAATTCGAAGCAGCCATAGATAGCGACTTTCCAAATTATCAGGTGCCCAT	5400
CTATCTTTCATACTTTACAACAAATGTCTGTCACTACTCAAAGCAATGC	5450
ATATGGCTTAGATCTCAACTCACACCCCGAGGATCCTAAAGGGATTGCT	5500
TTTTATTCTAATGTTTTTGGATGGTTTGATTTATTTCTAACTTGAAGTT	5550
ATTAATCTTGTACCAGAACCAAGATGTGACAGATGAAAACGCTGAAACTC	5600
TCACAATACTTATCGAACTTTTTATCGAAAGAGCAACTCAATGGTCTGAG	5650
GTCATTCACACCATAAGCTGCCTAGATGTCCTGAGATCTTTTGCAATCGC	5700
AGCAAGTCTCTGCTGGAAGCATGGCCAGGCTGTTATTTTTCCCGAAT	5750
CAGAAGCTACAGATCAGAATCAGAAAACAAAAGGGCCAATACTTAAATC	5800
CAAGGACTATGGCATCCATTTGCAGTTGCAGCCGATGGTCAATTGCCTGT	5850
TCCGAATGATATACTCCTTGGCGAGGCTAGAAGAAGCAGTGGCAGCATTC	5900
ATCCTCGGTCAATTGTTACTGACGGGACCAACATGGGCGGAAAATCAACT	5950
CTTCTTCGTGCAACATGTCTGGCCGTTATCTTTGCCCAAGTTTGTATACT	6000
CGTTAGATAATTACTCTATTCTTTGCAATCAGTTCTTCAACATGAATAAT	6050
AAATTCTGTTTTCTGTCTGCAGCTTGGCTGCTACGTGCCGTGTGAGTCTT	6100
GCGAAATCTCCCTCGTGGATACTATCTTACAAGGCTTGGCGCATCTGAT	6150

FIG. 11C

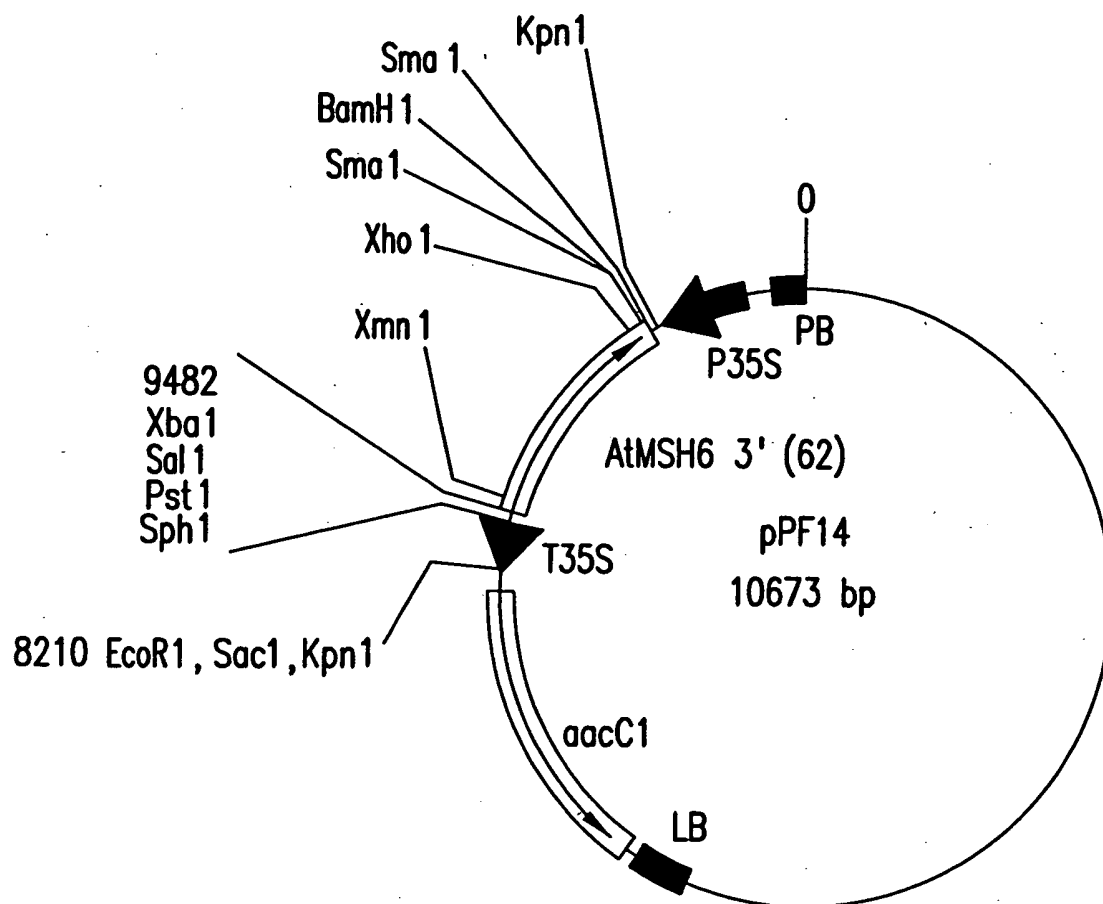
AGAATCATGACAGGAGAGAGTAAGTTTTGTTCTCAAAATACCAATTCCTC	6200
GAAC TATTTACTCAGATTTTGTCTGATTGGACAAGGTGGTTTTGCTTTTT	6250
TTTAGGTACCTTTTTGGTAGAATGCACTGAGACAGCGTCAGTTCTTCAGA	6300
ATGCAACTCAGGATTCAGTAGTAATCCTTGACGAACTGGGCAGAGGAACT	6350
AGTACTTTTCGATGGATACGCCATTGCATACTCGGTAACCTGCTCTTCTCC	6400
TTCAACTTATACTTGTGATCAACAAAAACATGCAATTCATTTTGCTGAA	6450
ACTTATTGATTTATATCAGGTTTTTCGTCACCTGGTAGAGAAAGTTCAAT	6500
GTCGGATGCTCTTTGCAACACATTACCACCCTCTCACCAAGGAATTCGCG	6550
TCTCACCCACGTGTCACCTCGAAACACATGGCTTGCGCATTCAAATCAAG	6600
ATCTGATTATCAACCACGTGGTTGTGATCAAGACCTAGTGTTCTTGTACC	6650
GTTTAACCGAGGGAGCTTGTCTGAGAGCTACGGACTTCAAGTGGCACTC	6700
ATGGCTGGAATACCAAACCAAGTGGTTGAAACAGCATCAGGTGCTGCTCA	6750
AGCCATGAAGAGATCAATTGGGGAAAACCTCAAGTCAAGTGAGCTAAGAT	6800
CTGAGTTCTCAAGTCTGCATGAAGACTGGCTCAAGTCATTGGTGGGTATT	6850
TCTCGAGTCGCCCACAACAATGCCCCATTGGCGAAGATGACTACGACAC	6900
TTTGTTTTGCTTATGGCATGAGATCAAATCCTCTTACTGTGTTCCCAAAT	6950
AAATGGCTATGACATAACACTATCTGAAGCTCGTTAAGTCTTTTGCTTCT	7000
CTGATGTTTATTCCTCTTAAAAAATGCTTATATATCAAAAAATTGTTTCC	7050
TCGATTATAACAAGATTATATATGTATCTGTCTGGTTTAGCTATGGTATAT	7100
AATATATGTATGTTTCATGAGATTGGTCAAGAGAAATACTCACAAACAGTA	7150
TATTAAGAAGGAAATATGTTTATGCATTAATTTAAGTTTCAAGATAAACT	7200
GCAAATAACCTCGACTAAAGTTGCAAAGACCAAACACAAATTACAAAAC	7250
TATAAGACTTAAGTTCTGAATTCCTAAAACCAAAAAAAAAAACAGAAC	7300
TATTTTGTTGCATCTACAAACAACACAAACCTACATAGTTTATAACTTAC	7350
TCATCACTGAGATTAACATCAGAATCATTCTCCATTTCTTCATCTTCACT	7400
CTCATCATCATCACCACCACCATGATGATTCTCCTCCTCTTCACGTAACC	7450
TAGCAATCTCACTCTGAGCTCTATCAACAATCTGCTTCTTCTGCAACTCC	7500
AAATCTCTCTGAAAATCAGCTCTCATCTTCTCCAACCTCCTTCATTTGCTC	7550
TTTCTTACTCTTCTCCATCTTCTATAAACCTTCCCAAACCTCTCAACAG	7600
AATCCGCCAACATCTTATACGAAGCAGCGTCATTAACCTTCTTCTCTCG	7650
TACTCAACCTCATCATCCTCATCCTCCTCCTCTTCAGAATCACCAGGACT	7700
ATCCATCATCTCATCAAACCCATTAGACTTATCTAAATAAACCTTAGTGT	7750
TCATAAACACAAACTCACCTGAATCAACACCACAAGCTAAACCTAAATCC	7800
GACTTGGGCGAAACACAAAGCAACATATCCAACCTATTGAAAAACGACCA	7850
TTTACTTGAACCTAAACCTGATTTCTCAACCTTAATCTTCTTTTTCTAT	7900
ACTTCTCTTCAAGTCATCAATCATTCTCCTACATTGCGTCTCAGATTTCT	7950
TCCATCCTTAGCTCCTCACTCACTTTCTCAGCTACTTCATTCCAATCCTC	8000
GTTCTCAAACCTCCTTCTACCCAATTGCAAAAAACCTATCTCCCAAACTT	8050
CAAGCAACACAA	8062

FIG. 11D



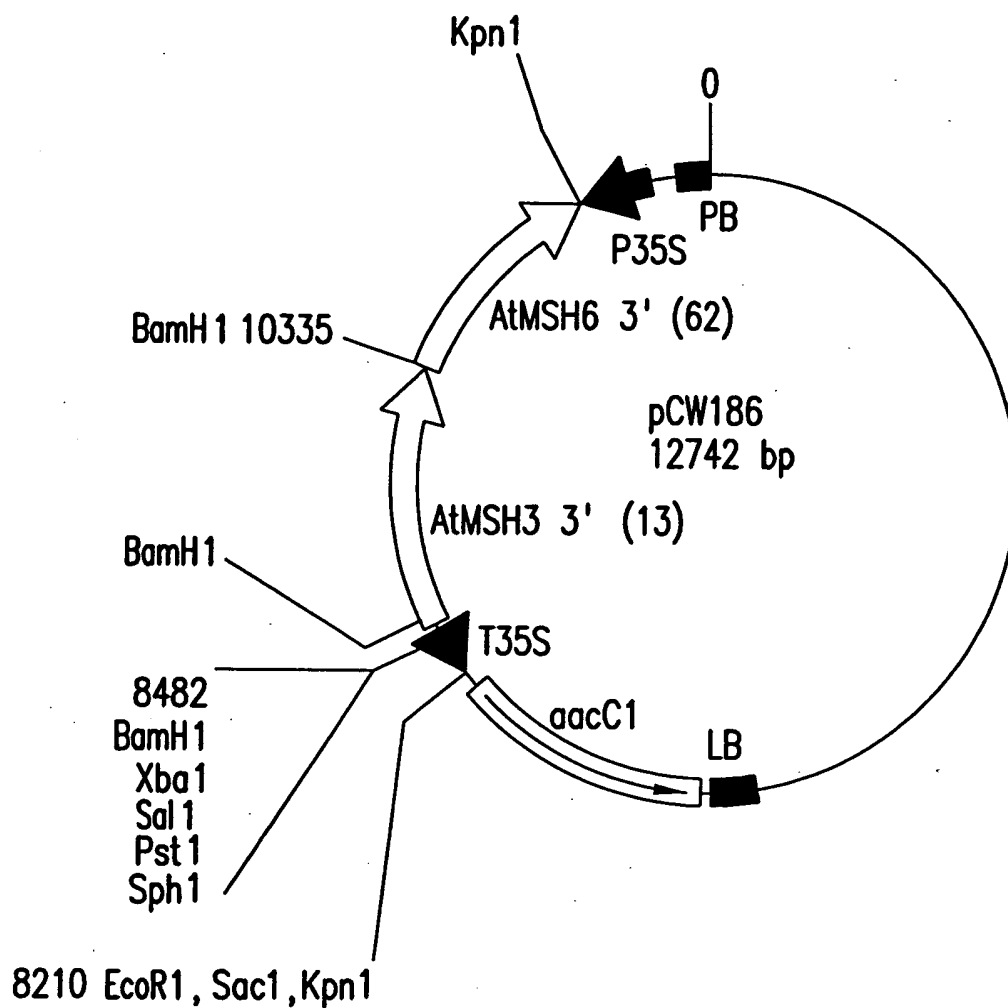
COMMENTS/REFERENCES: AtMSH3 3' SIDE ANTISENSE: AtMSH3 3' (13=2104bp) FROM pUC18/13 *Sal1*/*Sst1*/T4 INTO pCW164 *BamH1*/T4 IN AGROBACTERIUM LBA4404

FIG.12



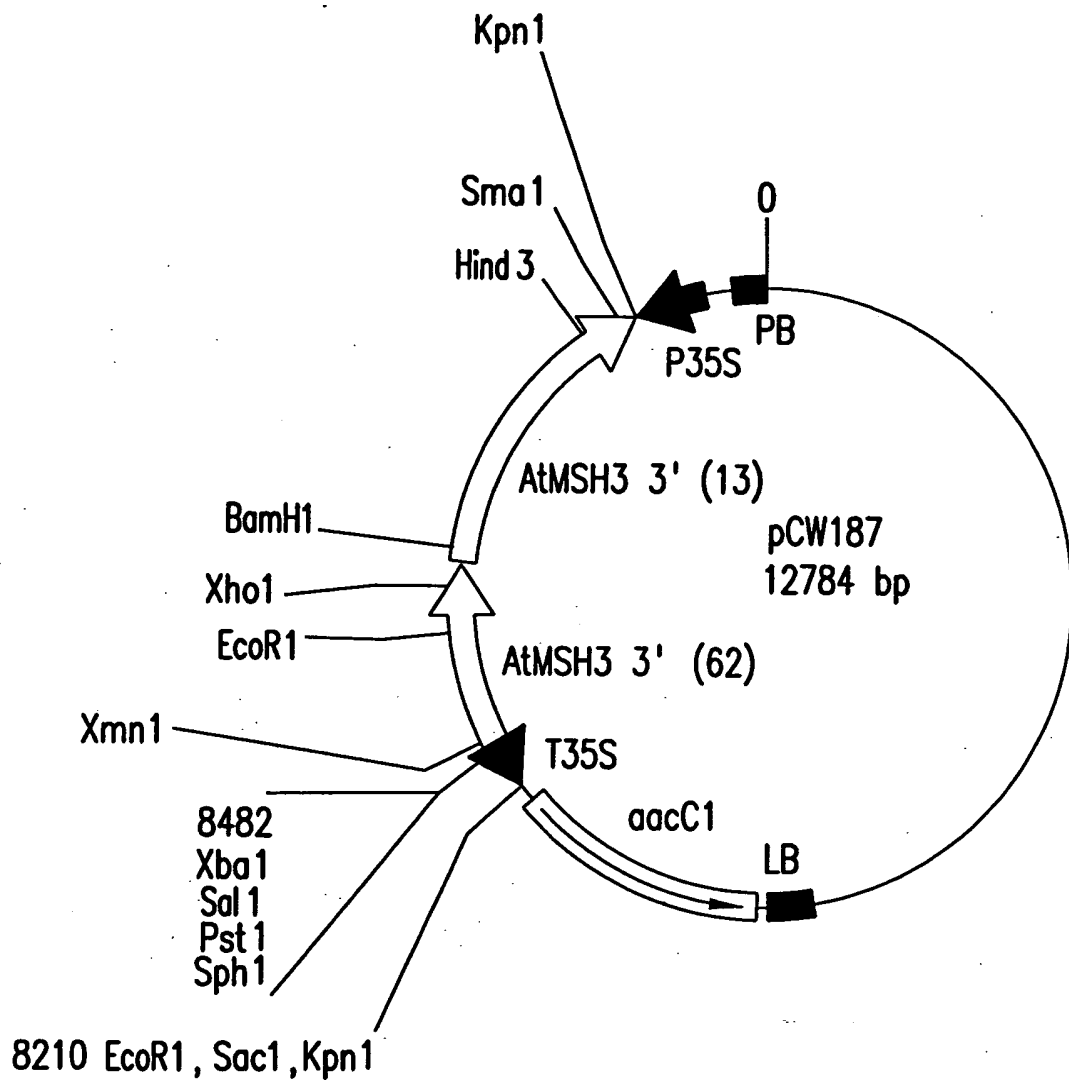
COMMENTS/REFERENCES: AtMSH6 (S8) 3' SIDE ANTISENS: 62 Sal1/Sst1/T4 (1379bp)
 INTO pCW164 BamH1/T4

FIG.13



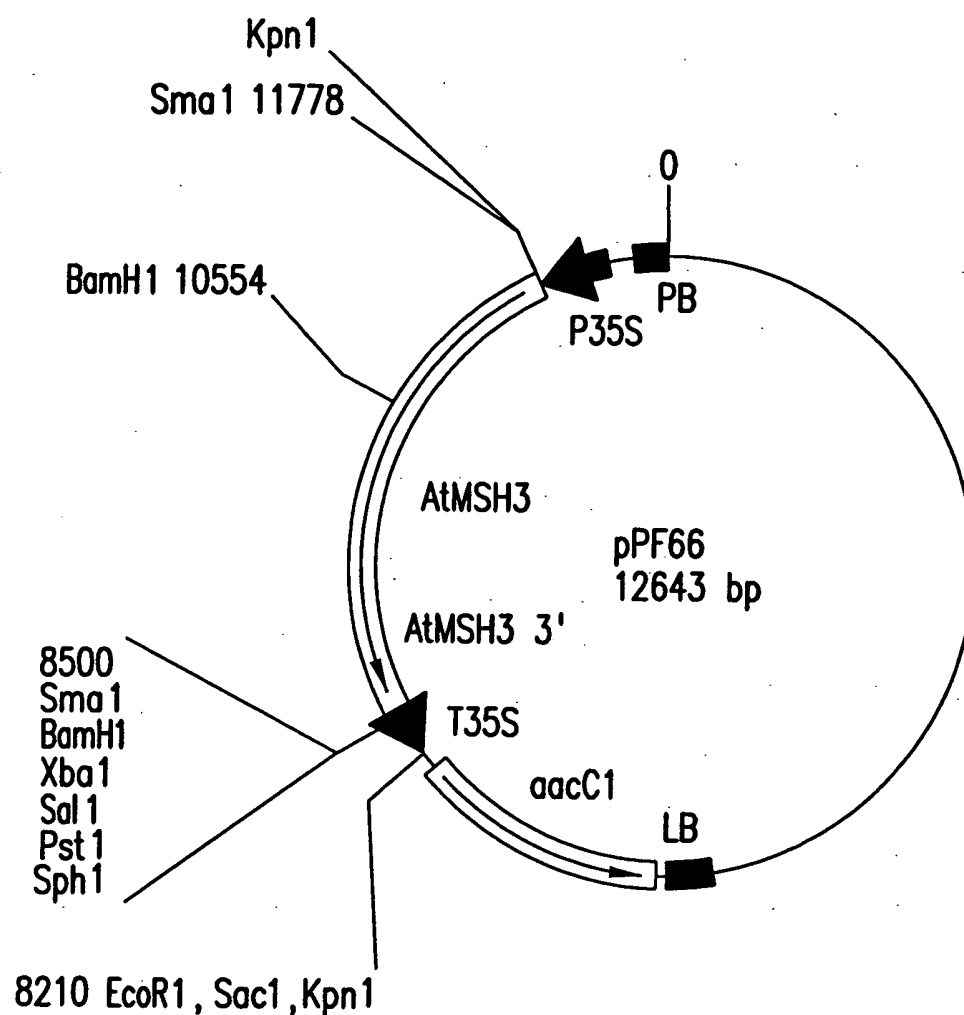
COMMENTS/REFERENCES: AtMSH6 3' /AtMSH3 3' ANTISENSE: AtMSH6 (S8) 3' SIDE (62=1379bp) Sal1/Sst1/T4 INTO pPF13 (pCW164 AtMSH3 (S5) 3' SIDE (13=2104) ANTISENS)/Sma1. IN LB4404

FIG.14



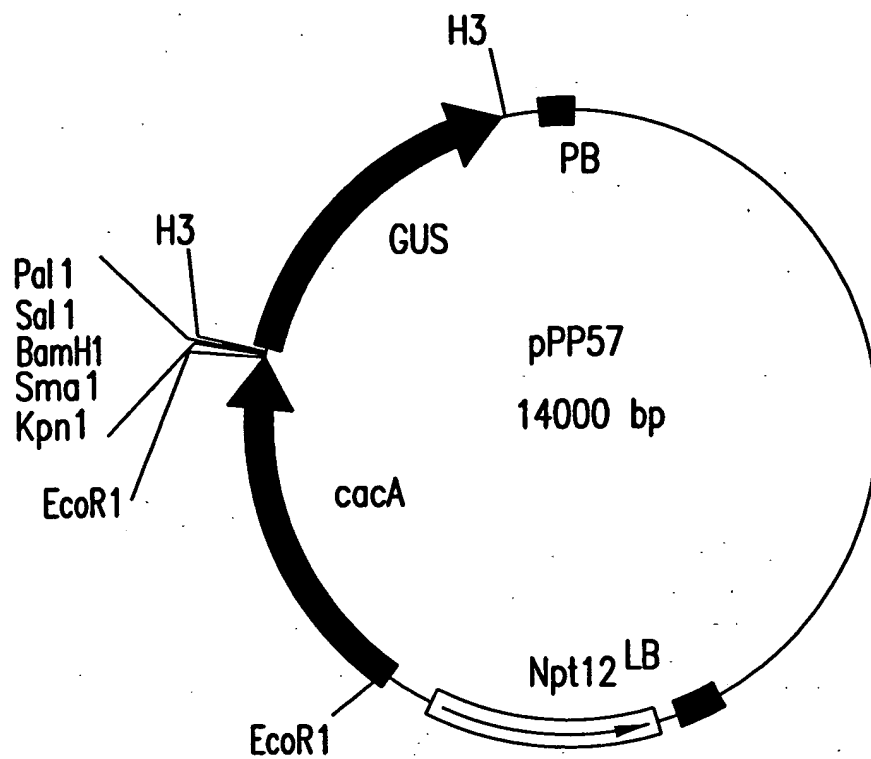
COMMENTS/REFERENCES: AtMSH3 3'/AtMSH6 3' ANTISENS (D): AtMSH3 (S5) 3' SIDE (13=2104bp) Sal1/Sst1/T4 INTO pPF14 (AtMSH6 (S8) 3' SIDE (62=1379bp) ANTISENSE INTO pCW164)/Sma1. IN LBA4404

FIG.15



COMMENTS/REFERENCES: AtMSH3 (S8) COMPLETE, SENSE ORIENTATION: pPF26 (3342bp)
Sma1 INTO pCW164 Sma1

FIG.16



COMMENTS/REFERENCES: pP2P111 WITH *codA* EcoR1 CASSETTE IN EcoR1 SITE AND Hind3 GUS CASSETTE IN Hind3 SITE KanR. ALL GENES UNDER PROMOTER/TERMINATOR 35S

FIG.17

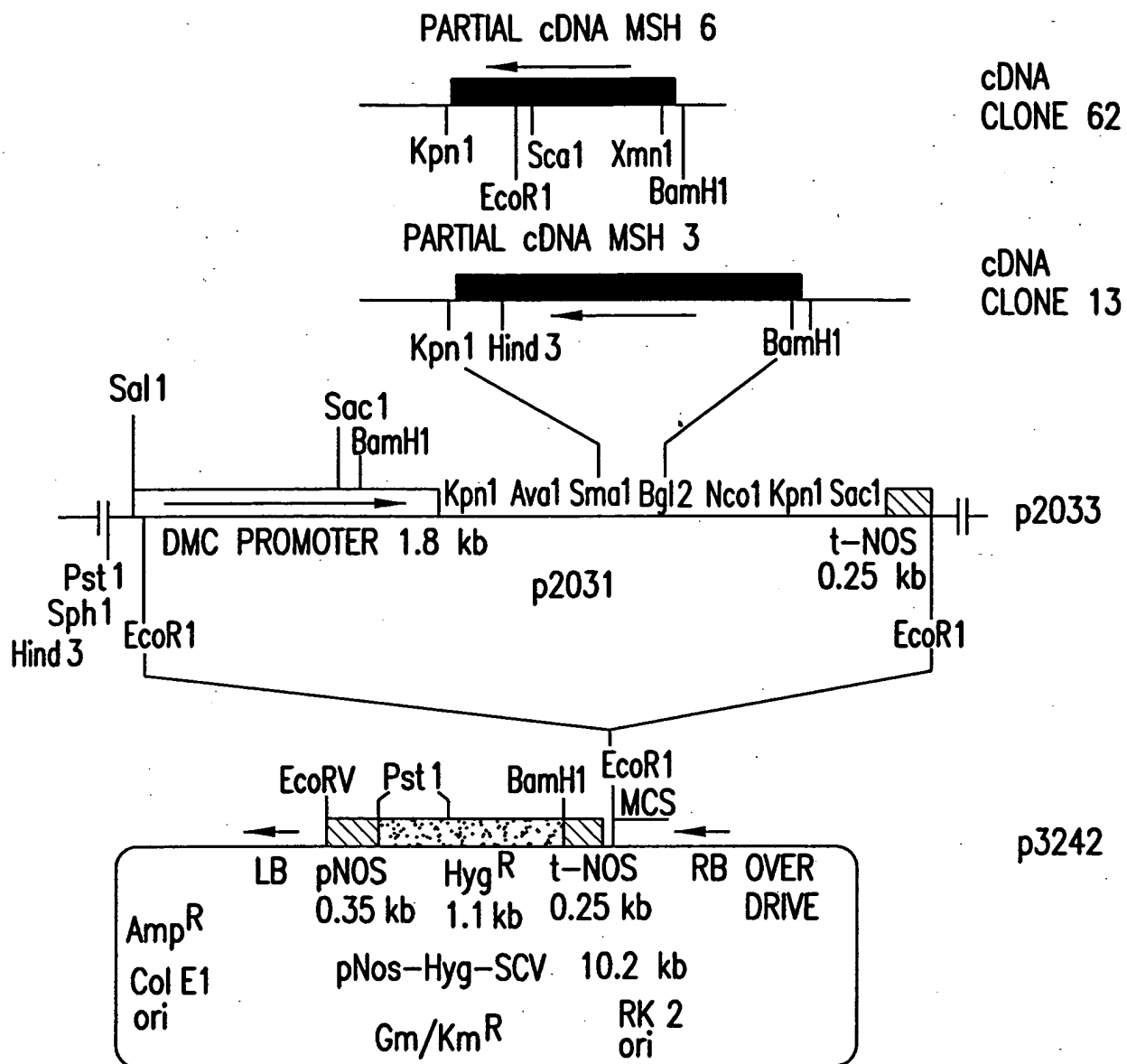


FIG.18

p3243

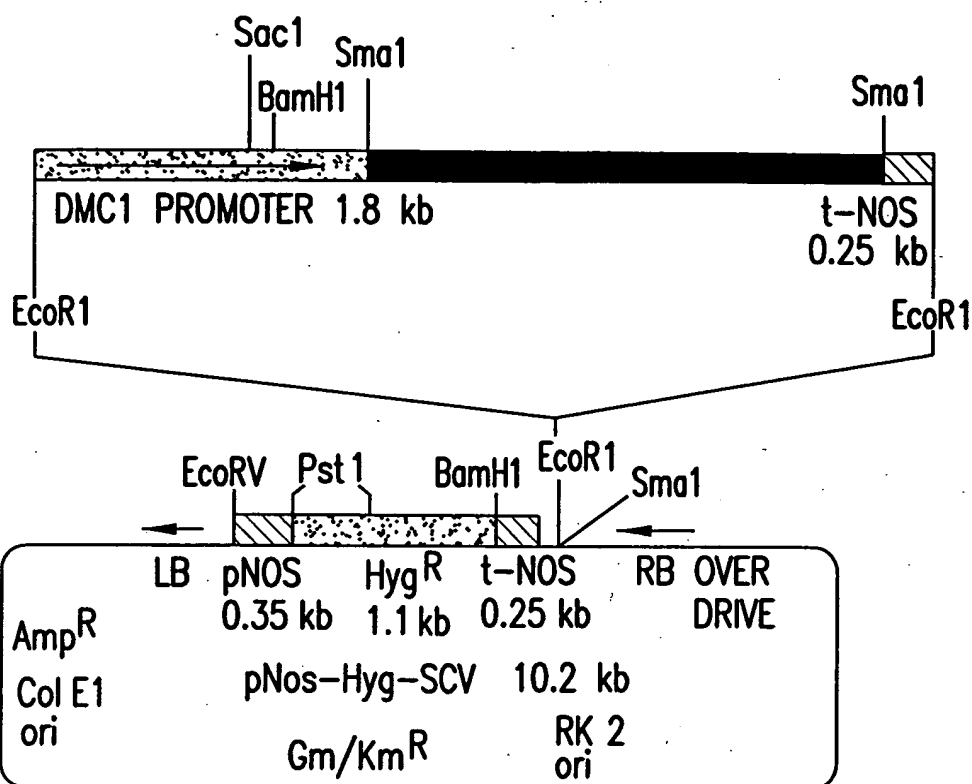


FIG.19